Jason J. Evans

Bioinformatics Engineer and Data Scientist

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Highlights

- **15+ years work experience applying bioinformatics in biotechnology, academic, clinical settings**
- **10+ years experience support and development in a CAP/CLIA genetic testing laboratory setting**
- **Designed and implemented variant calling and annotation pipelines for integration of exome and genome sequencing into clinical lab workflows**
- **Skilled on a Linux command-line for transform, merge, and extraction of complex data to reduce key information that is digestable to lab scientists and geneticists alike**

Education

University of Wisconsin-Madison **Madison, WI**
Bachelors of Science, Botany *1999*

Medical College of Wisconsin and Marquette University **Milwaukee, WI**
Masters of Science, Joint Program in Bioinformatics *2009*

Experience

Quest Diagnostics **Marlborough, MA**

Sr. Manager, Bioinformatics, Clinical Operations *12/2021-Current*

- Established a dedicated Clinical Operations group in support of Clinical Geneticists, Variant Scientists and Lab Operations within a CAP/CLIA regulatory setting
- Led development for cloud-based systems and the tools to register and find data, track provenance, and ease troubleshooting of cloud pipelines and supporting systems
- Drove extensible implementation of Python libraries to standardize logging, tracking, and connection between LIMS, cloud-based systems and interpretation and reporting databases
- Consolidated and simplified support of all of our systems used in our production clinical setting

Sr. Staff Scientist, Bioinformatics, Research & Development *7/2019-12/2021*

- Built first-in-kind long-read sequencing assay for quantification of tandem repeats for Ataxia diagnostic
- Built high-throughput whole exome pipeline for large scale consumer-based assay processing 100,000 samples per year

Sr. Scientist, Bioinformatics, Research & Development *1/2018-7/2019*

- Established the systems needed to scale from small targeted panel assays to assays using a Whole Exome Sequencing backbone for diagnostic use
- Produced Whole Exome Sequencing Copy Number Variant caller using a coverage-based approach

Courtagen Life Sciences **Woburn, MA**

Bioinformatics Scientist, Annotation & Interpretation *11/2015-7/2017*

- Support and implementation of interpretation and reporting web application providing feature improvements and bug fixes in a CAP/CLIA genetic testing environment
- Built web interface and backend to identify and queue variant confirmations using Sanger sequencing

Laboratory of Molecular Medicine/Partners Personalized Medicine **Cambridge, MA**

Bioinformatician *9/2012-11/2015*

- Produced end-to-end pipeline for distributed computation and variant calling for Whole Genome Sequencing in a CAP/CLIA genetic testing laboratory setting
- Implemented software to interface variant databases, variant annotation, and interpretation interfaces into a single, simple set of tools and resources

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Experience (con'd)

Harvard School of Public Health, Bioinformatics Core **Boston, MA**
Bioinformatician *7/2011-8/2012*

- Provided bioinformatics analyses and reports in support of contracting labs throughout HSPS
- Extensive contribution of tools and workflows towards the HSPS fork of the Galaxy Project

Marquette University, School of Biology **Milwaukee, WI**
Research Associate, Molecular Biology *5/2007-1/2008*

- Built molecular biology constructs for RNA Interference in *Chlamydomonas*

Applied Biosystems **Foster City, CA**
Bioinformatics Scientist *5/2001-5/2005*

- Built the computational analysis and system to run it in support of SNPlex custom oligo array
- Assisted in development of the first ABI 7900 high-throughput qPCR platform. Provided continued improvements in basecalling for the ABI 3700 sequencing instrument
- Leveraged the Celera human genome draft to identify putative drug targets in collaboration with contracted pharmaceutical companies

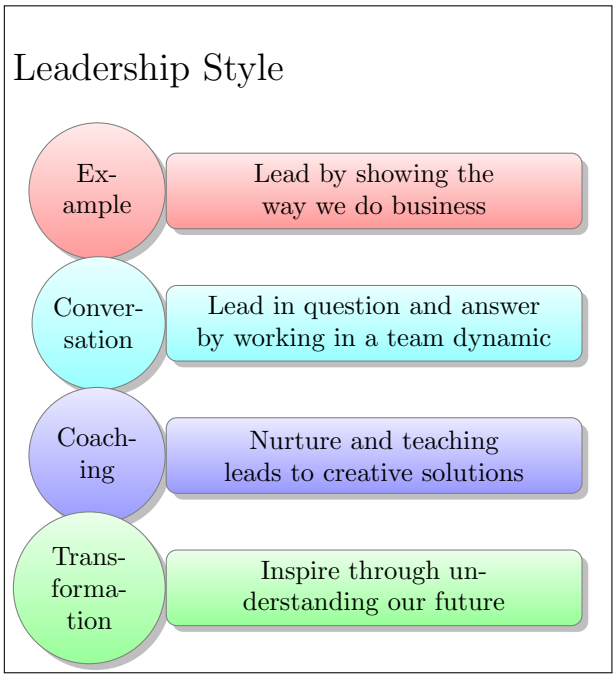
Celera Genomics **Foster City, CA**
Scientist *5/2000-5/2001*

- Wet lab identification of full-length cDNA clones targeting putative drug targets
- cDNA library archival in a high-throughput cloning laboratory focused on isolating drug targets identified by draft genome

Publications

Tsai, E.A.; Shakbatyan, R.; Evans, J.; Rossetti, P.; Graham, C.; Sharma, H.; Lin, C.-F.; Lebo, M.S. **Bioinformatics Workflow for Clinical Whole Genome Sequencing at Partners HealthCare Personalized Medicine**. J. Pers. Med. 2016, 6, 12.

Skills



Languages: STUFF
Developer Tools: STUFF
Technologies/Frameworks: STUFF